

RAW SEQUENCE LISTING

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Application Serial Number: 10/077,137A
Source: IFw16
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IFW16

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/077,137A

DATE: 06/20/2006

TIME: 16:00:35

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3 <110> APPLICANT: MACKAY, FABIENNE
 4 BROWNING, JEFFREY
 5 AMBROSE, CHRISTINE
 6 TSCHOPP, JURG
 7 SCHNEIDER, PASCAL
 8 THOMPSON, JEFFREY
 10 <120> TITLE OF INVENTION: BAFF RECEPTOR (BCMA), AN IMMUNOREGULATORY AGENT
 12 <130> FILE REFERENCE: 08201.0027
 14 <140> CURRENT APPLICATION NUMBER: 10/077,137A
 15 <141> CURRENT FILING DATE: 2005-02-15
 17 <150> PRIOR APPLICATION NUMBER: PCT/US00/22507
 18 <151> PRIOR FILING DATE: 2000-08-16
 20 <150> PRIOR APPLICATION NUMBER: 60/149,378
 21 <151> PRIOR FILING DATE: 1999-08-17
 23 <150> PRIOR APPLICATION NUMBER: 60/181,684
 24 <151> PRIOR FILING DATE: 2000-02-11
 26 <150> PRIOR APPLICATION NUMBER: 60/183,536
 27 <151> PRIOR FILING DATE: 2000-02-18
 29 <160> NUMBER OF SEQ ID NOS: 9
 31 <170> SOFTWARE: PatentIn Ver. 3.3
 33 <210> SEQ ID NO: 1
 34 <211> LENGTH: 184
 35 <212> TYPE: PRT
 36 <213> ORGANISM: Homo sapiens
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 42 Leu Leu His Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr
 43 20 25 30
 45 Pro Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser
 46 35 40 45
 48 Val Lys Gly Thr Asn Ala Ile Leu Trp Thr Cys Leu Gly Leu Ser Leu
 49 50 55 60
 51 Ile Ile Ser Leu Ala Val Phe Val Leu Met Phe Leu Leu Arg Lys Ile
 52 65 70 75 80
 54 Ser Ser Glu Pro Leu Lys Asp Glu Phe Lys Asn Thr Gly Ser Gly Leu
 55 85 90 95
 57 Leu Gly Met Ala Asn Ile Asp Leu Glu Lys Ser Arg Thr Gly Asp Glu
 58 100 105 110
 60 Ile Ile Leu Pro Arg Gly Leu Glu Tyr Thr Val Glu Glu Cys Thr Cys
 61 115 120 125
 63 Glu Asp Cys Ile Lys Ser Lys Pro Lys Val Asp Ser Asp His Cys Phe
 64 130 135 140

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66 Pro Leu Pro Ala Met Glu Glu Gly Ala Thr Ile Leu Val Thr Thr Lys
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 69 Thr Asn Asp Tyr Cys Lys Ser Leu Pro Ala Ala Leu Ser Ala Thr Glu
 70 165 170 175
 72 Ile Glu Lys Ser Ile Ser Ala Arg
 73 180
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 77 <211> LENGTH: 552
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 79 <213> ORGANISM: Homo sapiens
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 83 tgcatacctt gtcaacttcg atgttcttct aataactcctc ctcttaacatg tcaggattt 120
 84 gtaatgcaag tgtgaccaat tcagtgaaag gaacgaatgc gattctctgg acctgtttgg 180
 85 gactgagctt aataatttct ttggcagttt tcgtgctaattt gttttgcta aggaagataa 240
 86 gctctgaacc attaaaggac gagtttaaaa acacaggatc aggtctcctg ggcattggcta 300
 87 acattgaccc ggaaaagagc aggactggtg atgaaattat tctccgagag gcctcgagta 360
 88 cacggtgaa gaatgcaccc gtgaagactg catcaagagc aaaccgaagg tcgactctga 420
 89 ccattggctt ccactccggag ctatggagga aggccaaacc atttcttcac cacyaaaaacg 480
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 95 <211> LENGTH: 207
 96 <212> TYPE: PRT
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 103 Thr Gly Met Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe
 104 20 25 30
 106 Asp Ser Leu Asp Val Thr Met Leu Gln Met Ala Gly Gln Cys Ser Gln
 107 35 40 45
 109 Asn Glu Tyr Phe Asp Ser Leu Leu His Ala Cys Ile Pro Cys Gln Leu
 110 50 55 60
 112 Arg Cys Ser Ser Asn Thr Pro Pro Leu Thr Cys Leu His Ala Cys Ile
 113 65 70 75 80
 115 Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro Pro Leu Thr Cys Gln
 116 85 90 95
 118 Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val Lys Gly Gln Arg Tyr
 119 100 105 110
 121 Cys Asn Ala Ser Val Thr Asn Ser Val Lys Gly Val Asp Lys Thr His
 122 115 120 125
 124 Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
 125 130 135 140
 127 Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
 128 145 150 155 160
 130 Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
 131 165 170 175
 133 Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys

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 136 Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Tyr Val Val Ser Val
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 141 <211> LENGTH: 540
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 143 <213> ORGANISM: Homo sapiens
 145 <400> SEQUENCE: 4
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 147 gacgtcacga tggcgcagat ggctgggcag tgctccaaa atgaatattt tgacagttg 120
 148 ttgcgtgtt gcataacctg tcaacttcga tggttctcta atactcctcc tctaacaatgt 180
 149 cagcgttatt gtaatgcaag tggaccaat tcagtgaaag gaggcgacaa aactcacaca 240
 150 tgcccaccgt gcccagcacc tgaactcctg gggggaccgt cagtcttcct cttccccca 300
 151 aaaccccaagg acaccctcat gatctcccg acccctgagg tcacatgcgt ggtgggtggac 360
 152 gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat 420
 153 aatgccaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc 480
 154 ctcaccgtcc tgcaccagga ctggctgaat ggcaaggagt acaagtgcaa ggtctccaac 540
 157 <210> SEQ ID NO: 5
 158 <211> LENGTH: 140
 159 <212> TYPE: PRT
 160 <213> ORGANISM: Homo sapiens
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 166 Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
 167 20 25 30
 169 Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 170 35 40 45
 172 Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 173 50 55 60
 175 Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
 176 65 70 75 80
 178 Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
 179 85 90 95
 181 Gly Ser Phe Phe Lys Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
 182 100 105 110
 184 Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
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 187 Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 188 130 135 140
 191 <210> SEQ ID NO: 6
 192 <211> LENGTH: 369
 193 <212> TYPE: DNA
 194 <213> ORGANISM: Homo sapiens
 196 <400> SEQUENCE: 6
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 198 ccacagggtt acaccctgccc cccatcccg gatgagctga ccaagaacca ggtcagcctg 120
 199 acctgcctgg tcaaaggctt ctatcccagc gacatcgccg tggagtgaaa gagcaatggg 180
 200 cagccggaga acaactacaa gaccacgcct cccgtgttgg actccgacgg ctccttcttc 240

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 206 <210> SEQ ID NO: 7
 207 <211> LENGTH: 184
 208 <212> TYPE: PRT
 209 <213> ORGANISM: Homo sapiens
 211 <400> SEQUENCE: 7
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 213 1 5 10 15
 215 Leu Leu His Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr
 216 20 25 30
 218 Pro Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser
 219 35 40 45
 221 Val Lys Gly Thr Asn Ala Ile Leu Trp Thr Cys Leu Gly Leu Ser Leu
 222 50 55 60
 224 Ile Ile Ser Leu Ala Val Phe Val Leu Met Phe Leu Leu Arg Lys Ile
 225 65 70 75 80
 227 Ser Ser Glu Pro Leu Lys Asp Glu Phe Lys Asn Thr Gly Ser Gly Leu
 228 85 90 95
 230 Leu Gly Met Ala Asn Ile Asp Leu Glu Lys Ser Arg Thr Gly Asp Glu
 231 100 105 110
 233 Ile Ile Leu Pro Arg Gly Leu Glu Tyr Thr Val Glu Glu Cys Thr Cys
 234 115 120 125
 236 Glu Asp Cys Ile Lys Ser Lys Pro Lys Val Asp Ser Asp His Cys Phe
 237 130 135 140
 239 Pro Leu Pro Ala Met Glu Glu Gly Ala Thr Ile Leu Val Thr Thr Lys
 240 145 150 155 160
 242 Thr Asn Asp Tyr Cys Lys Ser Leu Pro Ala Ala Leu Ser Ala Thr Glu
 243 165 170 175
 245 Ile Glu Lys Ser Ile Ser Ala Arg
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 251 <212> TYPE: DNA
 252 <213> ORGANISM: Homo sapiens
 254 <400> SEQUENCE: 8
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 257 agctgctctt gctgcatttg ctctggatt cttgttagaga tattacttgt ccttccaggc 180
 258 ttttcttctt ttagctccct tttttcttt ttgtgatcat gttgcagatg gctgggcagt 240
 259 gctcccaaaa tgaatatttt gacagttgt tgcattgttgc cataccttgtt caacttcgtat 300
 260 gttcttctaa tactcctcct ctaacatgtc agcgttattt gttatgcattt gttgaccaatt 360
 261 cagtgaaagg aacgaatgcg attctctgga cctgtttggg actgagcttataatttctt 420
 262 tggcagttt cgtgctaattt tttttgtttaa ggaagataag ctctgaacca ttaaaggacg 480
 263 agtttaaaaa cacaggatca ggtctcttgg gcatggctaa cattgacccgtt gaaaagagca 540
 264 ggactggtga tggaaattttt cttccgagag gcctcgagta cacggtgaa gaatgcaccc 600
 265 gtgaagactg catcaagagc aaaccgaaagg tcgactctga ccattgctt ccactcccg 660
 266 ctatggagga aggcgcaacc attcttgcata ccacgaaaac gaatgactat tgcaagagcc 720

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267 tgccagctgc tttgagtgct acggagatag agaaatcaat ttctgctagg taattaaacca 780
 268 tttcgactcg agcagtgcct ctttaaaaat cttttgtcag aatagatgtat gtgtcagatc 840
 269 tcttttaggt gactgttattt ttctgtgcc gatacagctt tttgtcctct aactgtggaa 900
 270 actctttatg ttagatataat ttctcttaggt tactgttggg agcttaatgg tagaaaacttc 960
 271 cttggtttca tgattaaagt cttttttt cctga 995
 274 <210> SEQ ID NO: 9
 275 <211> LENGTH: 285
 276 <212> TYPE: PRT
 277 <213> ORGANISM: Homo sapiens
 279 <400> SEQUENCE: 9
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 281 1 5 10 15
 283 Lys Lys Arg Glu Glu Met Lys Leu Lys Glu Cys Val Ser Ile Leu Pro
 284 20 25 30
 286 Arg Lys Glu Ser Pro Ser Val Arg Ser Ser Lys Asp Gly Lys Leu Leu
 287 35 40 45
 289 Ala Ala Thr Leu Leu Leu Ala Leu Leu Ser Cys Cys Leu Thr Val Val
 290 50 55 60
 292 Ser Phe Tyr Gln Val Ala Ala Leu Gln Gly Asp Leu Ala Ser Leu Arg
 293 65 70 75 80
 295 Ala Glu Leu Gln Gly His His Ala Glu Lys Leu Pro Ala Gly Ala Gly
 296 85 90 95
 298 Ala Pro Lys Ala Gly Leu Glu Glu Ala Pro Ala Val Thr Ala Gly Leu
 299 100 105 110
 301 Lys Ile Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Asn
 302 115 120 125
 304 Ser Arg Asn Lys Arg Ala Val Gln Gly Pro Glu Glu Thr Val Thr Gln
 305 130 135 140
 307 Asp Cys Leu Gln Leu Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys
 308 145 150 155 160
 310 Gly Ser Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser
 311 165 170 175
 313 Ala Leu Glu Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr
 314 180 185 190
 316 Phe Phe Ile Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met
 317 195 200 205
 319 Gly His Leu Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu
 320 210 215 220
 322 Ser Leu Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu
 323 225 230 235 240
 325 Pro Asn Asn Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly
 326 245 250 255
 328 Asp Glu Leu Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu
 329 260 265 270
 331 Asp Gly Asp Val Thr Phe Phe Gly Ala Leu Lys Leu Leu
 332 275 280 285

VERIFICATION SUMMARY

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